

SEQUENCE LISTING

<110> Murphy, Erin E.
Mattson, Jeanine D.
Bates, Elizabeth Esther Mary
Gorman, Daniel M.
Lebecque, Serge J.E.

<120> Mammalian Genes; Related Reagents

<130> SF0818K

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<170> PatentIn Ver. 2.0

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-10

cca ggc ctg tgc ctg ctg tgc ctg gtg ttg gcg ctg cct gcc ctg ctg 164
Pro Gly Leu Ser Leu Leu Cys Leu Val Leu Ala Leu Pro Ala Leu Leu
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ccg gtg ccg gct gta cgc gga gtg gca gaa aca ccc acc tac ccc tgg 212
Pro Val Pro Ala Val Arg Gly Val Ala Glu Thr Pro Thr Tyr Pro Trp
15 20 25

cgg gac gca gag aca ggg gag cgg ctg gtg tgc gcc cag tgc ccc cca 260
Arg Asp Ala Glu Thr Gly Glu Arg Leu Val Cys Ala Gln Cys Pro Pro
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ggc acc ttt gtg cag cgg ccg tgc cgc cga gac agc ccc atg acg tgt 308
Gly Thr Phe Val Gln Arg Pro Cys Arg Arg Asp Ser Pro Met Thr Cys

A2
Cm:+

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Gly Pro Cys Pro Pro Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu			
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cgc tgc cgc twc tgc tac gtc ctc tgc ggg gag cgt gag gag gag gca			404
Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly Glu Arg Glu Glu Glu Ala			
80	85		90
cgg gct tgc cac gcc acc cac aac cgt gcc tgc cgc tgc cgc acc ggc			452
Arg Ala Cys His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly			
95	100		105
ttc ttc gcg cac gct ggt ttc tgc ttg gag cac gca tgc tgt cca cct			500
Phe Phe Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro			
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ggt gcc ggc gtg att gcc ccg ggc acc ccc agc cag aac acg cag tgc			548
Gly Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys			
125	130		135
cag ccg tgc ccc cca ggc acc ttc tca gcc agc agc tcc agc tca gag			596
Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser Glu			
140	145		155
cag tgc cag ccc cac cgc aac tgc acg gcc ctg ggc ctg gcc ctc aat			644
Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala Leu Asn			
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gtg cca ggc tct tcc tcc cat gac acc ctg tgc acc agc tgc act ggc			692
Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys Thr Gly			
175	180		185
ttc ccc ctc agc acc agg gta cca gga gct gag gag tgt gag cgt gcc			740
Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu Arg Ala			
190	195		200
gtc atc gac ttt gtg gct ttc cag gac atc tcc atc aag agg ctg cag			788
Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg Leu Gln			
205	210		215
cgg ctg ctg cag gcc ctc gag gcc ccg gag ggc tgg ggt ccg aca cca			836
Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu Gly Trp Gly Pro Thr Pro			
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agg gcg ggc cgc gcg gcc ttg cag ctg aag ctg cgt cgg cgg ctc acg			884
Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys Leu Arg Arg Arg Leu Thr			
240	245		250
gag ctc ctg ggg gcg cag gac ggg gcg ctg ctg gtg cgg ctg ctg cag			932
Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu Leu Val Arg Leu Leu Gln			
255	260		265
gcg ctg cgc gtg gcc agg atg ccc ggg ctg gag cgg agc gtc cgt gag			980
Ala Leu Arg Val Ala Arg Met Pro Gly Leu Glu Arg Ser Val Arg Glu			
270	275		280

A2
Cm.t

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Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
 40 45 50

Asp Ser Pro Met Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
 55 60 65

Phe Trp Asn Tyr Leu Glu Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly
 70 75 80 85

Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
 90 95 100

Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
 105 110 115

His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
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Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala
 135 140 145

Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
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Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
 170 175 180

Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
 185 190 195

Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
 200 205 210

Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu

A2
 com.t

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 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
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 cccgcctgg gcggccgccc cgctgggcag gtgctgagcg cccctagagc ctccttgcc 240
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A2
 Cmt

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Met Gly Thr Ser Pro
-40

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Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg Arg Ala
-35 -30 -25

aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc ctt agc 512
Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe Leu Ser
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tac cgc cat gtt gac cgt gcc acc ggc cag gtg cta acc tgt gac aag 608
Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys Asp Lys
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Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr Ser Cys
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gcg tct gkc agc agt tgc cct gtg ggg acc ttt acc agg cat gag aat 704
Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn
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ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg cca atg 752
Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met
65 70 75

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Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys
80 85 90

cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat acg gtg 848
Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val
95 100 105

tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg aca gag act gag gat 896
Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp
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gtg cgg tgt aag cag tgt gct cgg ggg tac ttc tca gat gtg cct tct 944
Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe Ser Asp Val Pro Ser
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agt gtg atg aan gca aag cat aca cag act gtc tgg atc aga acn tgg 992
Ser Val Met Xaa Ala Lys His Thr Gln Thr Val Trp Ile Arg Xaa Trp
145 150 155

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A2
Cm. +

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Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

Thr Asn Thr Ser Cys Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe
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Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
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Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe
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cggcttctcc ccgcctgggc ggccgcgcg ctgggcaggt gctgagcgcc cctagcgct 240
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tgggctcccg gcccgagg cgccggtgga tgcggcgctg ggcagaagca gccgccgatt 360
ccagctgccc cgcgcgcccc gggcgccct gcgagtcgcc gggtcagcc atg ggg acc 418
Met Gly Thr
-40

tct ccg agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc 466
Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg
-35 -30 -25

cga gcc aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc 514
Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe
-20 -15 -10

ctt agc acc acc aca gct cag cca gaa cag aag gcc tcg aat ctc att 562
Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile
-5 -1 1 5 10

ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg cta acc tgt 610
Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys
15 20 25

gac aag tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca 658
Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr
30 35 40

agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt acc agg cat 706
Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His
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gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg 754
Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp
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cca atg att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc 802
Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys
75 80 85 90

act tgc cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat 850
Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His
95 100 105

A2
cm.t

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gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc tca gat gtg 946
 Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val
 125 130 135

cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt ctg agt cag 994
 Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln
 140 145 150

aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac aac gtc tgt 1042
 Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val Cys
 155 160 165

ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc cct ggc aca 1090
 Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro Gly Thr
 175 180 185

gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa gtc cct tcc 1138
 Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu Val Pro Ser
 190 195 200

tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc aac tct tct 1186
 Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser Asn Ser Ser
 205 210 215

gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa ggg aca gtc 1234
 Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu Gly Thr Val
 220 225 230

cct gac aac aca agc tca gca agg ggg aag gaa gac gtg aac aag acc 1282
 Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val Asn Lys Thr
 235 240 245 250

ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc cac cac aga 1330
 Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro His His Arg
 255 260 265

cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg ggc gag aag 1378
 His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly Gly Glu Lys
 270 275 280

tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct aga cag aac 1426
 Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro Arg Gln Asn
 285 290 295

cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg atg att gtg 1474
 Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp Met Ile Val
 300 305 310

ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc agt atc cgg 1522
 Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys Ser Ile Arg
 315 320 325 330

aaa agc tcg agg act ctg aaa aag ggg ccc cgg cag gat ccc agt gcc 1570

A2
 cm.T

Lys	Ser	Ser	Arg	Thr	Leu	Lys	Lys	Gly	Pro	Arg	Gln	Asp	Pro	Ser	Ala		
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Ile	Val	Glu	Lys	Ala	Gly	Leu	Lys	Lys	Ser	Met	Thr	Pro	Thr	Gln	Asn		
			350					355					360				
cgg	gag	aaa	tgg	atc	tac	tac	tgc	aat	ggc	cat	ggt	atc	gat	atc	ctg		1666
Arg	Glu	Lys	Trp	Ile	Tyr	Tyr	Cys	Asn	Gly	His	Gly	Ile	Asp	Ile	Leu		
		365					370					375					
aag	ctt	gta	gca	gcc	caa	gtg	gga	agc	cag	tgg	aaa	gat	atc	tat	cag		1714
Lys	Leu	Val	Ala	Ala	Gln	Val	Gly	Ser	Gln	Trp	Lys	Asp	Ile	Tyr	Gln		
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Phe	Leu	Cys	Asn	Ala	Ser	Glu	Arg	Glu	Val	Ala	Ala	Phe	Ser	Asn	Gly		
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tac	aca	gcc	gac	cac	gag	cgg	gcc	tac	gca	gct	ctg	cag	cac	tgg	acc		1810
Tyr	Thr	Ala	Asp	His	Glu	Arg	Ala	Tyr	Ala	Ala	Leu	Gln	His	Trp	Thr		
				415					420					425			
atc	cgg	ggc	ccc	gag	gcc	agc	ctc	gcc	cag	cta	att	agc	gcc	ctg	cgc		1858
Ile	Arg	Gly	Pro	Glu	Ala	Ser	Leu	Ala	Gln	Leu	Ile	Ser	Ala	Leu	Arg		
			430					435					440				
cag	cac	cgg	aga	aac	gat	gtt	gtg	gag	aag	att	cgt	ggg	ctg	atg	gaa		1906
Gln	His	Arg	Arg	Asn	Asp	Val	Val	Glu	Lys	Ile	Arg	Gly	Leu	Met	Glu		
			445				450					455					
gac	acc	acc	cag	ctg	gaa	act	gac	aaa	cta	gct	ctc	ccg	atg	agc	ccc		1954
Asp	Thr	Thr	Gln	Leu	Glu	Thr	Asp	Lys	Leu	Ala	Leu	Pro	Met	Ser	Pro		
			460			465					470						
agc	ccg	ctt	agc	ccg	agc	ccc	atc	ccc	agc	ccc	aac	gcg	aaa	ctt	gag		2002
Ser	Pro	Leu	Ser	Pro	Ser	Pro	Ile	Pro	Ser	Pro	Asn	Ala	Lys	Leu	Glu		
					480				485					490			
aat	tcc	gct	ctc	ctg	acg	gtg	gag	cct	tcc	cca	cag	gac	aag	aac	aag		2050
Asn	Ser	Ala	Leu	Leu	Thr	Val	Glu	Pro	Ser	Pro	Gln	Asp	Lys	Asn	Lys		
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ggc	ttc	ttc	gtg	gat	gag	tgc	gag	ccc	ctt	ctc	cgc	tgt	gac	tct	aca		2098
Gly	Phe	Phe	Val	Asp	Glu	Ser	Glu	Pro	Leu	Leu	Arg	Cys	Asp	Ser	Thr		
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tcc	agc	ggc	tcc	tcc	gcg	ctg	agc	agg	aac	ggt	tcc	ttt	att	acc	aaa		2146
Ser	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys		
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gaa	aag	aag	gac	aca	gtg	ttg	cgg	cag	gta	cgc	ctg	gac	ccc	tgt	gac		2194
Glu	Lys	Lys	Asp	Thr	Val	Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp		
			540			545					550						
ttg	cag	cct	atc	ttt	gat	gac	atg	ctc	cac	ttt	cta	aat	cct	gag	gag		2242
Leu	Gln	Pro	Ile	Phe	Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu		
					555		560			565					570		

A2
Cm.T

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 575 580 585

cta ttc gaa att att gga gtc aag agc cag gaa gcc agc cag acc ctc 2338
 Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu
 590 595 600

ctg gac tct gtt tat agc cat ctt cct gac ctg ctg tagaacatag 2384
 Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
 605 610

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 10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
 25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
 40 45 50 55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
 60 65 70

A2
 cm't

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 75 80 85
 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
 90 95 100
 Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
 105 110 115
 Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
 120 125 130 135
 Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
 140 145 150
 Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
 155 160 165
 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
 170 175 180
 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
 185 190 195
 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
 200 205 210 215
 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
 220 225 230
 Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
 235 240 245
 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
 250 255 260
 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
 265 270 275
 Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
 280 285 290 295
 Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
 300 305 310
 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
 315 320 325
 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
 330 335 340
 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
 345 350 355
 Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile
 360 365 370 375

A2
 Cmt

Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp
 380 385 390
 Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe
 395 400 405
 Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln
 410 415 420
 His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser
 425 430 435
 Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly
 440 445 450 455
 Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro
 460 465 470
 Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala
 475 480 485
 Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp
 490 495 500
 Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys
 505 510 515
 Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe
 520 525 530 535
 Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp
 540 545 550
 Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn
 555 560 565
 Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys
 570 575 580
 Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser
 585 590 595
 Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
 600 605 610

<210> 7
 <211> 1474
 <212> DNA
 <213> primate

<220>
 <221> CDS
 <222> (1)..(1332)

<220>
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 <222> (124)..(1332)

A2
 Cm.†

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Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

atc gcc cgc cga gcc aca gcc acg atg atc gcg ggc tcc ctt ctc ctg 96
Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag gcc tgc 144
Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg 192
Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

cta acc tgt gac aag tgt cca gca gga acc tat gtc tct gag cat tgt 240
Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt 288
Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca 336
Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg act gac 384
Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85

cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct acc tgt 432
Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg 480
Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc 528
Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120 125 130 135

tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt 576
Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
140 145 150

ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac 624
Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
155 160 165

aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc 672
Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
170 175 180

A2
Cm't

cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa 720
 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
 185 190 195

gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc 768
 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
 200 205 210 215

aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa 816
 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
 220 225 230

ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa gac gtg 864
 Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
 235 240 245

aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc 912
 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
 250 255 260

cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg 960
 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
 265 270 275

ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct 1008
 Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
 280 285 290 295

aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg 1056
 Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
 300 305 310

atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc 1104
 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
 315 320 325

agt atc cgg aaa agc tgc agg act ctg aaa aag ggg ccc cgg cag gat 1152
 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
 330 335 340

ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca 1200
 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
 345 350 355

acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat gga ccc 1248
 Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro
 360 365 370 375

cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat 1296
 His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr
 380 385 390

att caa aga agc aat caa gat tca gaa aga tgg ggt tgataatttt 1342
 Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly
 395 400

tacttcaccc tgggaggcag catagtgcag tgaaaggat cgatatcctg aagcttgtag 1402

A2
 cm 4

cagcccaagt gggaagccag tggaagata tctatcagtt tctttgcaat gccagtgaga 1462
 gggaggttgc tg 1474

<210> 8
 <211> 444
 <212> PRT
 <213> primate

<400> 8
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 -40 -35 -30

Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
 -25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
 -5 -1 1 5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
 10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
 25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
 40 45 50 55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
 60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
 75 80 85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
 90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
 105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
 120 125 130 135

Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
 140 145 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
 155 160 165

Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
 170 175 180

Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
 185 190 195

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
 200 205 210 215

A2
 Cmt

Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
220 225 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
235 240 245

Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
250 255 260

His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
265 270 275

Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
280 285 290 295

Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
300 305 310

Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
315 320 325

Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
330 335 340

Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
345 350 355

Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro
360 365 370 375

His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr
380 385 390

Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly
395 400

<210> 9

<211> 227

<212> PRT

<213> rodent

<400> 9

Met Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu
1 5 10 15

Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr
20 25 30

Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp
35 40 45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val
50 55 60

Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu
65 70 75 80

A2
Gen 14

Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser
85 90 95

Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr
100 105 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala
115 120 125

Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys
130 135 140

Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn
145 150 155 160

Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser
165 170 175

Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile
180 185 190

Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr
195 200 205

Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr
210 215 220

Arg Ser Gln
225

<210> 10
<211> 225
<212> PRT
<213> primate

<400> 10
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

A2
omit

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150- 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220

Gln
225

<210> 11
<211> 187
<212> PRT
<213> primate

<400> 11
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

A2
Cm.t

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly
180 185

<210> 12
<211> 636
<212> DNA
<213> rodent

<220>
<221> CDS
<222> (104)..(553)

<220>
<221> mat_peptide
<222> (191)..(553)

<400> 12
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cagcactggc gagtagcagg aataaacacg tttggtgaga gcc atg gca ctc aag 115
Met Ala Leu Lys

gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc cta 163
Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu
-25 -20 -15 -10

ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg cag 211
Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg Gln
-5 -1 1 5

cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag tgc 259
Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys
10 15 20

gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
25 30 35

gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355
Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp Trp
40 45 50 55

ggg ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac cgc 403
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg
60 65 70

ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg gac 451
Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp
75 80 85

A2
Cm't

tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa gac 499
 Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp
 90 95 100

atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca cac 547
 Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His
 105 110 115

tgt gag tgatgtgccca agtggcagca gacctttaa aaaaaaagaa aaaaaaaca 603
 Cys Glu
 120

acaaaaaaca aaaaaaaaaa aaaaaaaaaa aaa 636

<210> 13
 <211> 150
 <212> PRT
 <213> rodent

A2
 Cm.t
 <400> 13
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 -25 -20 -15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 -10 -5 -1 1

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 5 10 15

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 20 25 30 35

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 40 45 50

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 55 60 65

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 70 75 80

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 85 90 95

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 100 105 110 115

Tyr Glu Pro His Cys Glu
 120

<210> 14
 <211> 474
 <212> DNA
 <213> primate

<220>

<221> CDS
<222> (78)..(473)

<220>
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<222> (308)
<223> N; may be A, C, G, or T

<220>
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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
30 35 40

A2
Cm.t

tgc cct cct cgc agt aca aaa gca gct ggg gcc acc aca aat gtc aga 254
 Cys Pro Pro Arg Ser Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg
 45 50 55

gtt gca tca cct gtg ctg tca tca atc gtg ttc aga agg ttc aac tgc 302
 Val Ala Ser Pro Val Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys
 60 65 70 75

aca gtn acc tct nat gct gtc tgt ggg gga ngg ttt gcc caa gtt tct 350
 Thr Xaa Thr Ser Xaa Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser
 80 85 90

aac cga aag aca cgc cat tgg aag gct gcc agg acc aag gat ggc atc 398
 Asn Arg Lys Thr Arg His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile
 95 100 105

ccg tgg cac aaa gnc aga ccc cca act tct gan ggt tnc aaa gtg nct 446
 Pro Trp His Lys Xaa Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa
 110 115 120

ttc caa ttg gag ctt aat ggg agg can a 474
 Phe Gln Leu Glu Leu Asn Gly Arg Xaa
 125 130

<210> 15
 <211> 132
 <212> PRT
 <213> primate

<400> 15
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1 5 10 15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
 20 25 30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Ser
 35 40 45

Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg Val Ala Ser Pro Val
 50 55 60

Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys Thr Xaa Thr Ser Xaa
 65 70 75 80

Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser Asn Arg Lys Thr Arg
 85 90 95

His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile Pro Trp His Lys Xaa
 100 105 110

Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa Phe Gln Leu Glu Leu
 115 120 125

Asn Gly Arg Xaa
 130

A2
 Cmut

<210> 16
<211> 546
<212> DNA
<213> primate

<220>
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<222> (78)..(308)

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<222> (317)
<223> N; may be A, C, G, or T

<220>
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<222> (340)
<223> N; may be A, C, G, or T

<220>
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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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<222> (429)
<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

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<223> N; may be A, C, G, or T

<220>
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<222> (468)

A2
Cm 4

<223> N; may be A, C, G, or T

<220>

<221> misc_feature

<222> (483)

<223> N; may be A, C, G, or T

<220>

<221> misc_feature

<222> (534)

<223> N; may be A, C, G, or T

<220>

<221> misc_feature

<222> (541)

<223> N; may be A, C, G, or T

<400> 16

cgcgctgagg tggatttgta ccggagtgccc atttgggagc aagagccatc tactcggtccg 60

ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc acà gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
30 35 40

tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
45 50 55

agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc caa ctg 302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu
60 65 70 75

cac agc taacctctna tgctgtctgt ggggatgttt gncccaagtt ctnaccgaaa 358
His Ser

agacacgccca tgggaagggt ggcaggacca ngaatggccn tcccgtggca gaaagccaga 418

ccccccaacn nctgnagggt ccaatgtggc cttncatttt ggaagcttan tgggaaggca 478

gatgncaacc caaagtggcc ccttcaggga ggccaaaatt tggtggcaat ggggtgnagca 538

gcntgccca 546

<210> 17

<211> 77

<212> PRT

<213> primate

<400> 17

A2
cm⁺

Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1 5 10 15
 Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
 20 25 30
 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
 35 40 45
 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50 55 60
 Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu His Ser
 65 70 75

<210> 18
 <211> 932
 <212> DNA
 <213> primate

<220>
 <221> CDS
 <222> (78)..(770)
 <220>
 <221> misc_feature
 <222> (782)
 <223> N; may be A, C, G, or T

<400> 18
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 ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
 1 5 10
 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
 15 20 25
 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
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 Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
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 Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys
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 Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr
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A2
 Cmt

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 Leu Val Glu Ala Asp Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu
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 Val Ala Leu Val Ser Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu
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 Arg Gly Gly Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu
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 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys

A2
 Cmt

50

55

60

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Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
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Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
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Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
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Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
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Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro
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Gln Gln Gln Gly Pro Glu Met
225 230

A2
Cmcd.